IFWO

RAW SEQUENCE LISTING   DATE: 10/15/2004
PATENT APPLICATION: US/10/734,661A   TIME: 11:07:01

        Input Set : **N:\AMC\US10734661A.raw**
        Output Set: **N:\CRF4\10152004\J734661A.raw**

```
 1 <110> APPLICANT: ProChon Biotech, Ltd.
 2        MorphoSys AG
 3        Yayon, Avner
 4        Thomassen-Wolf, Elisabeth
 5        Rom, Eran
 6        Borges, Eric
 7 <120> TITLE OF INVENTION: ANTIBODIES THAT BLOCK RECEPTOR PROTEIN TYROSINE KINASE
ACTIVATION
 8 <130> FILE REFERENCE: 81408-4400
 9 <140> CURRENT APPLICATION NUMBER: US/10/734,661A
10 <141> CURRENT FILING DATE: 2003-12-15
11 <150> PRIOR APPLICATION NUMBER: US 60/299,187
12 <151> PRIOR FILING DATE: 2001-06-20
13 <150> PRIOR APPLICATION NUMBER: PCT/IL02/00494
14 <151> PRIOR FILING DATE: 2002-06-20
15 <160> NUMBER OF SEQ ID NOS: 106
16 <170> SOFTWARE: PatentIn version 3.2
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 806
20 <212> TYPE: PRT
21 <213> ORGANISM: Homo sapiens
22 <300> PUBLICATION INFORMATION:
23 <308> DATABASE ACCESSION NO: np_000133
24 <309> DATABASE ENTRY DATE: 2001-02-21
25 <313> RELEVANT RESIDUES: (1)..(806)
26 <400> SEQUENCE: 1
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29     Val Ala Gly Ala Ser Ser Glu Ser Leu Gly Thr Glu Gln Arg Val Val
30                     20                  25                  30
31     Gly Arg Ala Ala Glu Val Pro Gly Pro Glu Pro Gly Gln Gln Glu Gln
32                     35                  40                  45
33     Leu Val Phe Gly Ser Gly Asp Ala Val Glu Leu Ser Cys Pro Pro Pro
34             50                  55                  60
35     Gly Gly Gly Pro Met Gly Pro Thr Val Trp Val Lys Asp Gly Thr Gly
36     65                  70                  75                  80
37     Leu Val Pro Ser Glu Arg Val Leu Val Gly Pro Gln Arg Leu Gln Val
38                     85                  90                  95
39     Leu Asn Ala Ser His Glu Asp Ser Gly Ala Tyr Ser Cys Arg Gln Arg
40                     100                 105                 110
41     Leu Thr Gln Arg Val Leu Cys His Phe Ser Val Arg Val Thr Asp Ala
42                     115                 120                 125
43     Pro Ser Ser Gly Asp Asp Glu Asp Gly Glu Asp Glu Ala Glu Asp Thr
44                     130                 135                 140
```

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P.6

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45   Gly Val Asp Thr Gly Ala Pro Tyr Trp Thr Arg Pro Glu Arg Met Asp
46   145                 150                 155                 160
47   Lys Lys Leu Leu Ala Val Pro Ala Ala Asn Thr Val Arg Phe Arg Cys
48                   165                 170                 175
49   Pro Ala Ala Gly Asn Pro Thr Pro Ser Ile Ser Trp Leu Lys Asn Gly
50                   180                 185                 190
51   Arg Glu Phe Arg Gly Glu His Arg Ile Gly Gly Ile Lys Leu Arg His
52                   195                 200                 205
53   Gln Gln Trp Ser Leu Val Met Glu Ser Val Val Pro Ser Asp Arg Gly
54       210                 215                 220
55   Asn Tyr Thr Cys Val Val Glu Asn Lys Phe Gly Ser Ile Arg Gln Thr
56   225                 230                 235                 240
57   Tyr Thr Leu Asp Val Leu Glu Arg Ser Pro His Arg Pro Ile Leu Gln
58                   245                 250                 255
59   Ala Gly Leu Pro Ala Asn Gln Thr Ala Val Leu Gly Ser Asp Val Glu
60                   260                 265                 270
61   Phe His Cys Lys Val Tyr Ser Asp Ala Gln Pro His Ile Gln Trp Leu
62       275                 280                 285
63   Lys His Val Glu Val Asn Gly Ser Lys Val Gly Pro Asp Gly Thr Pro
64       290                 295                 300
65   Tyr Val Thr Val Leu Lys Thr Ala Gly Ala Asn Thr Thr Asp Lys Glu
66   305                 310                 315                 320
67   Leu Glu Val Leu Ser Leu His Asn Val Thr Phe Glu Asp Ala Gly Glu
68                   325                 330                 335
69   Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Phe Ser His His Ser Ala
70                   340                 345                 350
71   Trp Leu Val Val Leu Pro Ala Glu Glu Glu Leu Val Glu Ala Asp Glu
72       355                 360                 365
73   Ala Gly Ser Val Tyr Ala Gly Ile Leu Ser Tyr Gly Val Gly Phe Phe
74       370                 375                 380
75   Leu Phe Ile Leu Val Val Ala Ala Val Thr Leu Cys Arg Leu Arg Ser
76   385                 390                 395                 400
77   Pro Pro Lys Lys Gly Leu Gly Ser Pro Thr Val His Lys Ile Ser Arg
78                   405                 410                 415
79   Phe Pro Leu Lys Arg Gln Val Ser Leu Glu Ser Asn Ala Ser Met Ser
80                   420                 425                 430
81   Ser Asn Thr Pro Leu Val Arg Ile Ala Arg Leu Ser Ser Gly Glu Gly
82       435                 440                 445
83   Pro Thr Leu Ala Asn Val Ser Glu Leu Glu Leu Pro Ala Asp Pro Lys
84       450                 455                 460
85   Trp Glu Leu Ser Arg Ala Arg Leu Thr Leu Gly Lys Pro Leu Gly Glu
86   465                 470                 475                 480
87   Gly Cys Phe Gly Gln Val Val Met Ala Glu Ala Ile Gly Ile Asp Lys
88                   485                 490                 495
89   Asp Arg Ala Ala Lys Pro Val Thr Val Ala Val Lys Met Leu Lys Asp
90                   500                 505                 510
91   Asp Ala Thr Asp Lys Asp Leu Ser Asp Leu Val Ser Glu Met Glu Met
92       515                 520                 525
93   Met Lys Met Ile Gly Lys His Lys Asn Ile Ile Asn Leu Leu Gly Ala
```

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Input Set : **N:\AMC\US10734661A.raw**
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```
 94          530              535              540
 95    Cys Thr Gln Gly Gly Pro Leu Tyr Val Leu Val Glu Tyr Ala Ala Lys
 96    545              550              555              560
 97    Gly Asn Leu Arg Glu Phe Leu Arg Ala Arg Arg Pro Pro Gly Leu Asp
 98                  565              570              575
 99    Tyr Ser Phe Asp Thr Cys Lys Pro Pro Glu Glu Gln Leu Thr Phe Lys
100                  580              585              590
101      Asp Leu Val Ser Cys Ala Tyr Gln Val Ala Arg Gly Met Glu Tyr Leu
102              595              600              605
103      Ala Ser Gln Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn Val Leu
104            610              615              620
105      Val Thr Glu Asp Asn Val Met Lys Ile Ala Asp Phe Gly Leu Ala Arg
106      625              630              635              640
107      Asp Val His Asn Leu Asp Tyr Tyr Lys Lys Thr Thr Asn Gly Arg Leu
108                  645              650              655
109      Pro Val Lys Trp Met Ala Pro Glu Ala Leu Phe Asp Arg Val Tyr Thr
110                  660              665              670
111      His Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu Ile Phe
112              675              680              685
113      Thr Leu Gly Gly Ser Pro Tyr Pro Gly Ile Pro Val Glu Glu Leu Phe
114       .690              695              700
115      Lys Leu Leu Lys Glu Gly His Arg Met Asp Lys Pro Ala Asn Cys Thr
116      705              710              715              720
117      His Asp Leu Tyr Met Ile Met Arg Glu Cys Trp His Ala Ala Pro Ser
118                  725              730              735
119      Gln Arg Pro Thr Phe Lys Gln Leu Val Glu Asp Leu Asp Arg Val Leu
120                  740              745              750
121      Thr Val Thr Ser Thr Asp Glu Tyr Leu Asp Leu Ser Ala Pro Phe Glu
122              755              760              765
123      Gln Tyr Ser Pro Gly Gly Gln Asp Thr Pro Ser Ser Ser Ser Ser Gly
124          770              775              780
125      Asp Asp Ser Val Phe Ala His Asp Leu Leu Pro Pro Ala Pro Pro Ser
126      785              790         .    795              800
127      Ser Gly Gly Ser Arg Thr
128                       805
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130 <210> SEQ ID NO: 2
131 <211> LENGTH: 32
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: artificial primer
136 <400> SEQUENCE: 2
137   acgtgctagc tgagtccttg gggacggagc ag   32
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140 <211> LENGTH: 55
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: artificial primer

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```
145 <400> SEQUENCE: 3
146       acgtctcgag ttaatggtga tggtgatggt gtgcatacac acagcccgcc tcgtc        55

148 <210> SEQ ID NO: 4
149 <211> LENGTH: 1147
150 <212> TYPE: DNA
151 <213> ORGANISM: Homo sapiens
152 <300> PUBLICATION INFORMATION:
153 <308> DATABASE ACCESSION NO: m58051
154 <309> DATABASE ENTRY DATE: 1994-11-08
155 <313> RELEVANT RESIDUES: (1)..(1147)
156 <400> SEQUENCE: 4
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158       tcgcgctctg cgtggccgtg gccatcgtgg ccggcgcctc ctcggagtcc ttggggacgg    120
159       agcagcgcgt cgtggggcga gcggcagaag tcccgggccc agagcccggc cagcaggagc    180
160       agttggtctt cggcagcggg gatgctgtgg agctgagctg tccccgccc ggggtggtc    240
161       ccatggggcc cactgtctgg gtcaaggatg gcacagggct ggtgccctcg gagcgtgtcc    300
162       tggtggggcc ccagcggctg caggtgctga atgcctccca cgaggactcc ggggcctaca    360
163       gctgccggca gcggctcacg cagcgcgtac tgtgccactt cagtgtgcgg gtgacagacg    420
164       ctccatcctc gggagatgac gaagacgggg aggacgaggc tgaggacaca ggtgtggaca    480
165       caggggcccc ttactggaca cggcccgagc ggatggacaa gaagctgctg gccgtgccgg    540
166       ccgccaacac cgtccgcttc cgctgcccag ccgctggcaa ccccactccc tccatctcct    600
167       ggctgaagaa cggcagggag ttccgcggcg agcaccgcat tggaggcatc aagctgcggc    660
168       atcagcagtg gagcctggtc atggaaagcg tggtgccctc ggaccgcggc aactacacct    720
169       gcgtcgtgga gaacaagttt ggcagcatcc ggcagacgta cacgctggac gtgctggagc    780
170       gctccccgca ccggcccatc ctgcaggcgg ggctgccggc caaccagacg gcggtgctgg    840
171       gcagcgacgt ggagttccac tgcaaggtgt acagtgacgc acagccccac atccagtggc    900
172       tcaagcacgt ggaggtgaac ggcagcaagg tgggcccgga cggcacaccc tacgttaccg    960
173       tgctcaagac ggcgggcgct aacaccaccg acaaggagct agaggttctc tccttgcaca   1020
174       acgtcacctt tgaggacgcc ggggagtaca cctgcctggc gggcaattct attgggtttt   1080
175       ctcatcactc tgcgtggctg gtggtgctgc cagccgagga ggagctggtg gaggctgacg   1140
176       aggcggg                                                             1147

178 <210> SEQ ID NO: 5
179 <211> LENGTH: 5695
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Expression Vector pCEP-PU/AC7
184 <400> SEQUENCE: 5
185       gacggatcgg gagatctccc gatcccctat ggtcgactct cagtacaatc tgctctgatg     60
186       ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg    120
187       cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc    180
188       ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt    240
189       gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata    300
190       tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc    360
191       cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc    420
192       attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt    480
193       atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt    540
194       atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca    600
195       tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg    660
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Input Set : N:\AMC\US10734661A.raw
Output Set: N:\CRF4\10152004\J734661A.raw

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197    aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg   780
198    gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca   840
199    ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc   900
200    gtttaaactt aagcttggta ccgagctcgg atccccgtcg tgcatctatc gaaggtcgtg   960
201    gagatcccga ggagcccaaa tcttgtgaca aaactcacac atgcccaccg tgcccagcac  1020
202    ctgaactcct ggggggaccg tcagtcttcc tcttcccccc aaaacccaag gacaccctca  1080
203    tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac gaagaccctg  1140
204    aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag acaaagccgc  1200
205    gggaggagca gtacaacagc acgtaccggg tggtcagcgt cctcaccgtc ctgcaccagg  1260
206    actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc ccagccccca  1320
207    tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg tacaccctgc  1380
208    ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg gtcaaaggct  1440
209    tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag aacaactaca  1500
210    agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc aagctcaccg  1560
211    tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg catgaggctc  1620
212    tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaatga tctagagggc  1680
213    ccgtttaaac ccgctgatca gcctcgactg tgccttctag ttgccagcca tctgttgttt  1740
214    gcccctcccc cgtgccttcc ttgaccctgg aaggtgccac tcccactgtc ctttcctaat  1800
215    aaaatgagga aattgcatcg cattgtctga gtaggtgtca ttctattctg gggggtgggg  1860
216    tggggcagga cagcaagggg gaggattggg aagacaatag caggcatgct ggggatgcgg  1920
217    tgggctctat ggcttctgag gcggaaagaa ccagctgggg ctctaggggg tatccccacg  1980
218    cgccctgtag cggcgcatta agcgcggcgg gtgtggtggt tacgcgcagc gtgaccgcta  2040
219    cacttgccag cgccctagcg cccgctcctt tcgctttctt cccttccttt ctcgccacgt  2100
220    tcgccggctt tccccgtcaa gctctaaatc ggggcatccc tttagggttc cgatttagtg  2160
221    ctttacggca cctcgacccc aaaaaacttg attagggtga tggttcacgt agtgggccat  2220
222    cgccctgata gacggttttt cgccctttga cgttggagtc cacgttcttt aatagtggac  2280
223    tcttgttcca aactggaaca acactcaacc ctatctcggt ctattctttt gatttataag  2340
224    ggattttggg gatttcggcc tattggttaa aaaatgagct gatttaacaa aaatttaacg  2400
225    cgaattaatt ctgtggaatg tgtgtcagtt agggtgtgga aagtccccag gctccccagg  2460
226    caggcagaag tatgcaaagc atgcatctca attagtcagc aaccaggtgt ggaaagtccc  2520
227    caggctcccc agcaggcaga agtatgcaaa gcatgcatct caattagtca gcaaccatag  2580
228    tcccgcccct aactccgccc atcccgcccc taactccgcc cagttccgcc cattctccgc  2640
229    cccatggctg actaattttt tttatttatg cagaggccga ggccgcctct gcctctgagc  2700
230    tattccagaa gtagtgagga ggcttttttg gaggcctagg cttttgcaaa aagctcccgg  2760
231    gagcttgtat atccattttc ggatctgatc agcacgtgtt gacaattaat catcggcata  2820
232    gtatatcggc atagtataat acgacaaggt gaggaactaa accatggcca gttgaccag  2880
233    tgccgttccg gtgctcaccg cgcgcgacgt cgccggagcg gtcgagttct ggaccgaccg  2940
234    gctcgggttc tcccgggact tcgtggagga cgacttcgcc ggtgtggtcc gggacgacgt  3000
235    gaccctgttc atcagcgcgg tccaggacca ggtggtgccg gacaacaccc tggcctgggt  3060
236    gtgggtgcgc ggcctggacg agctgtacgc cgagtggtcg gaggtcgtgt ccacgaactt  3120
237    ccgggacgcc tccgggccgg ccatgaccga gatcggcgag cagccgtggg ggcgggagtt  3180
238    cgccctgcgc gacccggccg gcaactgcgt gcacttcgtg gccgaggagc aggactgaca  3240
239    cgtgctacga gatttcgatt ccaccgccgc cttctatgaa aggttgggct cggaatcgt  3300
240    tttccgggac gccggctgga tgatcctcca gcgcggggat ctcatgctgg agttcttcgc  3360
241    ccaccccaac ttgtttattg cagcttataa tggttacaaa taaagcaata gcatcacaaa  3420
242    tttcacaaat aaagcatttt tttcactgca ttctagttgt ggtttgtcca aactcatcaa  3480
243    tgtatcttat catgtctgta taccgtcgac ctctagctag agcttggcgt aatcatggtc  3540
244    atagctgttt cctgtgtgaa attgttatcc gctcacaatt ccacacaaca tacgagccgg  3600
```

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            RAW SEQUENCE LISTING ERROR SUMMARY        DATE: 10/15/2004
            PATENT APPLICATION:  US/10/734,661A       TIME: 11:07:02

            Input Set : N:\AMC\US10734661A.raw
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```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

```
Seq#:54; N Pos. 253,254,255
Seq#:56; N Pos. 256,257,258
Seq#:70; N Pos. 1,2,3
Seq#:74; N Pos. 1,2,3
Seq#:81; N Pos. 1,2,3
Seq#:83; N Pos. 1,2,3
```

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

```
Seq#:1; Line(s) 7
Seq#:7; Line(s) 326
Seq#:30; Line(s) 580
Seq#:31; Line(s) 589
Seq#:32; Line(s) 598
Seq#:33; Line(s) 607
Seq#:34; Line(s) 616
Seq#:35; Line(s) 625
Seq#:36; Line(s) 634
Seq#:37; Line(s) 643
Seq#:38; Line(s) 652
Seq#:39; Line(s) 661
Seq#:40; Line(s) 670
Seq#:41; Line(s) 679
Seq#:42; Line(s) 688
Seq#:43; Line(s) 697
Seq#:44; Line(s) 706
Seq#:45; Line(s) 715
Seq#:46; Line(s) 724
Seq#:47; Line(s) 733
Seq#:48; Line(s) 742
Seq#:49; Line(s) 751
Seq#:50; Line(s) 760
Seq#:51; Line(s) 769
```

VERIFICATION SUMMARY   DATE: 10/15/2004
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```
L:9 M:270 C: Current Application Number differs, Wrong Format
L:984 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54 after pos.:240
L:1016 M:341 W: (46) "n" or "Xaa" used, for. SEQ ID#:56 after pos.:240
L:1212 M:341 W: (46)· "n" or "Xaa" used, for SEQ ID#:70 after pos.:0
L:1273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0
L:1380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0
L:1413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
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